

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 4, 2002, 01:57:45 ; Search time 24.7555 Seconds
(without alignments)
1429.075 Million cell updates/sec

Title: US-09-805-550-4

Perfect score: 1910
Sequence: 1 MKLTVKTLKGFHEIRVQPN.....CDRNEELANYLLHAGGED 368

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 segs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1153.5	60.4	379	2 T14337	RAD23 protein, iso
2	1043.5	54.6	367	2 F96827	protein F20B17.8 f
3	954	49.9	382	2 T14336	RAD23 protein, iso
4	887.5	46.5	392	2 T04150	RAD23 protein homo
5	661.5	34.6	246	2 G86296	T24D18.27 protein
6	640.5	33.5	385	2 JC7783	RAD 23B protein -
7	625.5	32.7	409	2 S44346	RAD23 protein homo
8	603.5	31.6	363	2 S44443	RAD23 protein homo
9	561.5	29.4	368	2 T40115	uv excision repair
10	424	22.2	113	2 H86296	F309.1 protein - A
11	405	21.2	372	2 T27774	hypothetical prote
12	403	21.1	398	2 S50507	excision repair pr
13	204.5	10.7	142	2 T51479	hypothetical prote
14	201	10.5	551	2 C84549	probable ubiquitin
15	195.5	10.2	536	2 B84549	probable ubiquitin
16	163.5	8.6	354	2 T38404	yeast dsk2 homolog
17	163.5	8.6	502	2 T18562	hypothetical prote
18	159	8.3	373	2 S54583	ubiquitin-like pro
19	143	7.5	324	2 T02358	ubiquitin homolog
20	140	7.3	701	2 J01674	ubiquitin-like fus
21	138	7.2	313	2 J01728	ubiquitin precursor
22	137.5	7.2	292	2 T18584	F15C11.2 - Caenorh
23	136	7.1	1135	2 T30561	Scytale protein - A
24	135	7.1	356	1 UQ07RC	polyubiquitin / ri
25	132.5	6.9	990	2 T14756	hypothetical prote
26	130.5	6.8	76	2 S31653	ubiquitin - giardi
27	127.5	6.7	80	2 T28305	ORF MSV144 probabl
28	126.5	6.6	77	2 S29238	ubiquitin - Entamo
29	126.5	6.6	156	1 UQ0H07	ubiquitin / riboso

30	126.5	6.6	156	1 I52328	ubiquitin / riboso
31	126.5	6.6	157	2 I50438	ubiquitin polyprot
32	126.5	6.6	167	2 I51568	ubiquitin - Af
33	126.5	6.6	222	1 UQHY	ubiquitin precursor
34	126.5	6.6	229	1 UQ0H07	ubiquitin precursor
35	126.5	6.6	229	1 S13928	ubiquitin precursor
36	126.5	6.6	231	1 A31560	polyubiquitin - It
37	126.5	6.6	245	2 A29584	ubiquitin - bo
38	126.5	6.6	255	2 A29584	ubiquitin precursor
39	126.5	6.6	305	1 S29853	polyubiquitin 4 -
40	126.5	6.6	305	1 I50437	polyubiquitin 4 -
41	126.5	6.6	305	1 S12583	polyubiquitin 4 -
42	126.5	6.6	361	2 S21083	polyubiquitin 5 -
43	126.5	6.6	685	1 UQ0H07	polyubiquitin 9 -
44	126.5	6.6	810	2 S45359	polyubiquitin 10 -
45	126	6.6	155	1 UQ0W7A	ubiquitin / riboso

ALIGNMENTS

RESULT 1

T14337
RAD23 protein, isoform II - carrot

C:Species: Daucus carota (carrot)

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000

C:Accession: T14337
R:Sturm, A.; Reinhard, S.
Plant J. 13, 815-821, 1998

A:Title: Two isoforms of plant RAD23 complement a UV-sensitive rad23 mutant in yeast.

A:Reference number: Z17989; MUID:98345997; PMID:9681019

A:Accession: T14337

A>Status: preliminary; translated from GH/EMBL/DDB

A:Molecule type: mRNA

A:Residues: 1-379 <SPU>

A:Cross-references: EMBL:Y12014; NID:91914684; PIDN:CAA72742.1; PID:91914685

A:Experimental source: subspecies Queen Anne's lace, isolate W001C

A:Genetics:

A:Gene: RAD23-2

C:Superfamily: unassigned ubiquitin-related proteins; ubiquitin homology.

Query Match	Score	DB 2;	Length	379;
Best Local Similarity	60.4%	Pred. No. 5.5e-70;		
Matches 240; Conservative 45; Mismatches 81; Indels 15; Gaps 9;				
QY 1	1	MKLTVKTLKGFHEIRVQPNDTMAVKNIEIQKDSYPMGQOLIFNGKVLKDESTLE 60		
DB 1	1	MKLTVKTLKGFHEIRVQPNDTMAVKNIEIQKDSYPMGQOLIFNGKVLKDESTLE 60		
QY 61	61	ENKYNEDGFLVYMLSKGTSGTSSQSHSNTPATROAP---PLEAPQOAPPPVAPIT 117		
DB 61	61	ESKISDEGFLVYMLSKGTSGTSTCPAAQSSAPRPAPVAPAPAPAPAPAPAPAPAP 120		
QY 118	118	TSQPEG--LPAQAP-NTHDNAASNLGSRNVDTIINDLEMGGSGWCKDYQALRAAYN 174		
DB 121	121	T-VEAPLSPAFAPSDTYGEAASNVVAGSNLEQIIOHIMDGCGMPTNNVSRALRAAYN 179		
QY 175	175	NPEAAVEYVSGIVTAETAIAPDIG---GQGANITDRA--PTGEAGLS-GIPNTAPDLFP 228		
DB 180	180	NPEAAVDTLYSGIPEMAAAPPVSHFQGDQINAAANNISDNGVGAAPGAPNSLPLNMF 239		
QY 229	229	QGASNAGGAGGGLDFLRNPPQFAVENVHTNPOLIPMLVLSKRONPOLILIEENH 288		
DB 240	240	QETLSGTVGAGLSGLEFLRNPPQFOTLRSMVQNRNPOLIPMLVLSKRONPOLILIEENH 299		
QY 289	289	DEFLQNLNPEPGEGLDQPEEDENPHAISVPEDEAIGRLSKGFDPRARYEAPLA 348		
DB 300	300	EEFLQNLNPEPGEGLDQPEEDENPHAISVPEDEAIGRLSKGFDPRARYEAPLA 358		
QY 349	349	CDRNEELANYLLHAGG-ED 368		
DB 359	359	CDRNEELANYLLHAGG-ED 379		

RESULT 2

F96827

protein F20B17.8 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 17-May-2002

C:Accession: F96827

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federpieli, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Jensen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Malt, R.; Marzilli, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: F96827

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-367 <STO>

A:Cross-references: GB:AEO05173; NID:97715605; PIDN:AAF68123.1; GSPDB:GNO0141

C:Genetics:

A:Gene: F20B17.8

A:Map position: 1

C:Superfamily: unassigned ubiquitin-related proteins; ubiquitin homology

Query Match 54.6%; Score 1043.5; DB 2; Length 367;

Best Local Similarity 59.3%; Pred. No. 1.2e-62;

Matches 232; Conservative 39; Mismatches 73; Indels 47; Gaps 11;

QY 1 MKLYTKTGHEIRVOQNDITMAVKNIEIOGDSYPMGQOLLIFNGKYLKDESTLE 60

DB 1 MKLYTKTGSHPEIRVLPDITMAVKNIEIOGDSYPMGQOLLIFNGKYLKDESTLE 60

QY 61 ENKVEDGFLVYMLSKGTSSTSSQ-----HSNTPATRQAPLEAQAQAPPV 113

DB 61 ENKVEEGFLVYMLSKGSGSAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 111

QY 114 APTT-----SOPEGLPAQAPNTHDNASNLGSRNVDTIINQIMEMGGGSMWDXV 165

DB 112 NFVETCSCTFYSCSRTG-----TDYGAQASTLVSGSLQEMVOQIMEMGGGSMWDXV 166

QY 166 QALAAVNNPRAVEYLYSGIPVTAETVY-----IGQGANTDRATGAGLSGTPN 220

DB 167 TRLRAATNNPRAVDYLYSGIPQTAETVYVPEAOIAGSGA-----APVAPR--SGPN 219

QY 221 TAPLDFPQAGSNAGGAGGGLDFLRNPNQFAVREMYHTNPQILQPMIVELSKONPQI 280

DB 220 SSPDLFPQETVAAGSGDLGTFELFRNNDQVALI--TISAFSLNCEPRMLQGLGKQNPQ 277

QY 281 LRLIENHDEFLQLINEPREG--GGGDFLDQPEDEMPHAIVTPEEOAIGRLSMDGF 338

DB 278 LRLIENHDEFLQLINEPREG--GGGDFLDQPEDEMPHAIVTPEEOAIGRLSMDGF 336

QY 339 RARVIEAFLACDRNEELAAVYLLHAGE-ED 368

DB 337 RALVIEAFLACDRNEELAAVYLLHAGE-ED 367

RESULT 3

T14336

RAD23 protein, isoform I - carrot

C:Species: Daucus carota (carrot)

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000

C:Accession: T14336

R:Sturm, A.; Leibhard, S.

A:Title: Two isoforms of plant RAD23 complement a UV-sensitive rad23 mutant in yeast.

A:Reference number: Z17989; MUID:96345997; PMID:9681019

A:Accession: T14336

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-382 <STO>

A:Cross-references: EMBL:Y12013; NID:91914682; PIDN:CAA72741.1; PID:91914683

A:Experimental source: subspecies Queen Anne's lace, isolate W001C

C:Genetics:

A:Gene: RAD23-1

C:Superfamily: unassigned ubiquitin-related proteins; ubiquitin homology

Query Match 49.9%; Score 954; DB 2; Length 382;

Best Local Similarity 52.4%; Pred. No. 1.3e-56;

Matches 205; Conservative 52; Mismatches 98; Indels 36; Gaps 9;

QY 1 MKLYTKTGHEIRVOQNDITMAVKNIEIOGDSYPMGQOLLIFNGKYLKDESTLE 60

DB 1 MKLYTKTGSHPEIRVLPDITMAVKNIEIOGDSYPMGQOLLIFNGKYLKDESTLE 60

QY 61 ENKVEDGFLVYMLSKGTSSTSSQSHSNTPATRQAPLEAQAQAPPV-OPVPA- 114

DB 61 ENNVANSTIVIMLSKSKSPSGSGSTTS-----TAAAPKAPQTSAPSPVAPAPVSPAST 116

QY 115 -PTTSQPGCLPAQAP-----NTHDNASNLGSRNVDTIINQIMEMGGGSMWDXD 163

DB 117 LPPAPSPAPAPATAPIPSAAGSEANVYDASAISILVAGSINLEGAIQIILDMGGGTWDRD 176

QY 164 KYORALRAAVNNPRAVEYLYSGIPVTAETVY-----GGGANTDRATG--EAGIS 216

DB 177 TVIRIVRAAFNNPRAVEYLYSGIPQAP-APPVAPSPSGAANLDPAPAAQAPAPAS 235

QY 217 GIPNTAPLDFPQAGSNAG--GAGAGGLDFLRNPNQFAVREMYHTNPQILQPMIVELSK 275

DB 236 AGPNANPRLDFPQGLPDMGSMNAGAGNDLFTNQFQALRMVQSNPQILQPMIVELSK 295

QY 276 QNPQILRLIENHDEFLQLINEPREGGDFLDQPEDEMPHAIVTPEEOAIGRLSMDGF 335

DB 296 QNPQILRLIENHDEFLQLINEPREGGDFLDQPEDEMPHAIVTPEEOAIGRLSMDGF 349

QY 336 GFDRAVIEAFLACDRNEELAAVYLLHAGE 366

DB 350 GFDRELIVIEVFRACNKEELAAVYLLHAGE 380

RESULT 4

RAD23 protein homolog - rice

C:Species: Oryza sativa (rice)

C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000

C:Accession: T04150

R:Schultz, T.F.; Quatrano, R.S.

A:Title: Characterization and expression of a rice RAD23 gene.

A:Reference number: Z08695; MUID:97369378; PMID:9225866

A:Accession: T04150

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-392 <SCH>

A:Cross-references: EMBL:U63530; NID:91488296; PIDN:AA65841.1; PID:91488297

A:Experimental source: cv. Nipponbare

C:Genetics:

A:Gene: RAD23

C:Superfamily: unassigned ubiquitin-related proteins; ubiquitin homology

Query Match 46.5%; Score 887.5; DB 2; Length 392;

Best Local Similarity 50.9%; Pred. No. 3.8e-52;

Matches 199; Conservative 52; Mismatches 109; Indels 31; Gaps 10;

QY 1 MKLYTKTGHEIRVOQNDITMAVKNIEIOGDSYPMGQOLLIFNGKYLKDESTLE 60

DB 1 MKISVTKLGSTFQIEVDSAGVADYKRIETTGQGHITPAEQMLIHGKYLKDESTLE 60

QY 61 ENKVEDGFLVYMLSKGTSSTSSQSHSNTPATRQAPLEAQAQAP--OPVAPITTT 118

DB 61 ENKVLNENFLVIMLQGGKSSSSAPATSK-----APSNQAPPIQTVPAPAPASQAPVAPATTT 116

QY 119 -----SOEGCLPAQAP-----NTHDNASNLLSGRNVDTITNQLMEMGGSGWDK 163
 Db 117 VPTVSAPTPTATAPASPAVASSEADNYSNLAAGSNLTLENTIQSILLEMGGIMVDR 176
 QY 164 KYORALRAAYNPERAVEYLYSGIPVTAETAVPIGQ-OGANTTDRA----PTGAGLSGI 218
 Db 177 IYVHALSAANNRERAVEYLYSGIPVPMQDIPVPPSPQAPNPQASATQPAASILSSG 236
 QY 219 PNTAPLDLPFGASNAGGAGG-GPLDPLRNNPQFQAVREMTNPQILQPMLEYSKON 277
 Db 237 PNASPLDLPFOALPNASTDAGLGNLDALRNNAQFRTLLSIVQNPQILQPLQELGKON 296
 QY 278 PQILRIEENHDEFLQNLNPEFG-GEQDFLDQ-PEEDDEPHALSYVPEQDEAGRLISM 335
 Db 297 PQILQIQEQAFLHLINEPABEGDEENLDQPE--AMPQTLAVPEDEALIRLEPM 354
 QY 336 GFDRAVTEAFACDRNEELAANYLLEHAGE 366
 Db 355 GFDRAVLVDVFFACNKDEQLAANYLLDHMNE 385

RESULT 5
 G86296
 T24D18.27 protein - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 27-Nov-2001
 C:Accession: G86296
 R:Theologas, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Com. L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
 ansen, N.F.; Hughes, B.; Hutzar, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lucros, J.S.; Maitl, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 Ker, M.; Wu, D.; Xu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: G86296
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-246 <STO>
 A:Cross-references: GB:AEO05172; NID:96587822; PIDN:AAF16513.1; GSPDB:GN00141
 C:Genetics:
 A:Map position: 1

Query Match 34.6%; Score 661.5; DB 2; Length 246;
 Best Local Similarity 56.7%; Pred. No. 2.9e-37;
 Matches 143; Conservative 29; Mismatches 63; Indels 17; Gaps 4;

QY 1 MKLTVKTLKGFHEIRVQPNMTIMAVKKNIEIGKDSYPMGQQLIFNGKVLKDESTLE 60
 Db 1 MKLTVKTLKGFHEIRVQPNMTIMAVKKNIEIGKDSYPMGQQLIFNGKVLKDESTLE 60
 QY 61 ENKYNEDGFLVYMLSKGTSGTSSQSHNTPATRQAPPLLEAPQAPPPVAPITTSQ 120
 Db 61 ENKYNEDGFLVYMLSKGTSGTSSQSHNTPATRQAPPLLEAPQAPPPVAPITTSQ 120
 QY 121 PEGPAQAPNTHDNAANLISGRNVDTITNQLMEMGGSGWDKQVORALRAAYNPERAV 180
 Db 109 VQEPQASQSDTYGQASTLVSSSIEQVQOIMEMGGSGWDKQVORALRAAYNPERAV 168
 QY 181 EYLYSGIPVTAETAVPIGQANTTDRAPTGEAGLSIPTAPLDLPFGASNAGGAG 239
 Db 169 DYLYSGIPVTAETAVPIGQANTTDRAPTGEAGLSIPTAPLDLPFGASNAGGAG 224
 QY 240 GGPIDFLRNPQ 251
 Db 225 LGTLEFLRGNDQ 236

RESULT 6
 JC7783

RAD 23B protein - channel catfish
 C:Species: Ictalurus punctatus (channel catfish)
 C>Date: 02-Apr-2002 #sequence_revision 02-Apr-2002 #text_change 02-Apr-2002
 C:Accession: JC7783
 R:Li, Z.; Li, P.; Kocabas, A.; Karsi, A.; Ju, Z.
 Biochem. Biophys. Res. Commun. 289, 317-324, 2001
 A:Title: Microsatellite-containing genes from the channel catfish brain: Evidence of
 A:Reference number: JC7783
 A:Contents: Brain
 A:Accession: JC7783
 A:Molecule type: mRNA
 A:Residues: 1-385 <LIU>
 C:Comment: This protein with a polypeptide tract, has importance in the nucleotide
 C:Genetics:
 A:Gene: rad23b
 A:Introns: 76/73

Query Match 33.5%; Score 640.5; DB 2; Length 385;
 Best Local Similarity 35.1%; Pred. No. 1.3e-35;
 Matches 142; Conservative 88; Mismatches 118; Indels 57; Gaps 9;

QY 1 MKLTVKTLKGFHEIRVQPNMTIMAVKKNIEIGKDSYPMGQQLIFNGKVLKDESTLE 60
 Db 1 MQTLTKLQOQTFKIDDAETVAKALEKIEKESFPYAGOKLILYAGKILNDTALK 60
 QY 61 ENKYNEDGFLVYMLSKGTSGTSSQSHNTPATRQAPPLLEAPQAPPPVAPITTSQ 114
 Db 61 EYKIDENKFNVMYAKPKATTAASSTTAASSSTSTTPVPPVAAATTTT 120
 QY 115 PITTSQ-----PEGCLPAQA-----PETHDNASNLLSGRNVDTITNQLM 153
 Db 121 TTTTSTSESSVIEKAEEKPSTSPASSGSLTNVIFERASALVTGGSYEMVVEIM 180
 QY 154 EMGGSGWDKQVORALRAAYNPERAVEYLYSGIPVTAETAVPIGQANTTD 206
 Db 181 LMG---YERREYVAAALASFPNPRAVEYLYTGIPVSEGVNAGSDPAAPVGGAPAYTT- 236
 QY 207 RAPTEAGLSGIPMTAPLDLPFGASNAGGAGGGLDPLRNNPQFQAVREMTNPQIL 266
 Db 237 -----GLSSPSTTP-----TQTAGSSGANPFLFNQPOFLQMRQIQQNPSL 281
 QY 267 QPMLEYSKONPQILRIEENHDEFLQNLNPEFG-GEQDFLDQ-PEEDDEPHALISVTP 323
 Db 282 PALLQIGRENPPOLLQSSHQEQFQMLNPEPAQAGGGGVSLEAGGGMNY-IGVTP 340
 QY 324 EEOGAIGLESMPFDRARVIAFLACDRNEELAANYLLEHAGEED 368
 Db 341 QEKALIERKALGPEGLVIAQVACRKNEMLANPILQONFDD 385

RESULT 7
 S44346
 RAD23 protein homolog - human
 N:Alternate names: p58/HR23B; XP-C repair complementing protein
 C:Species: Homo sapiens (man)
 C>Date: 25-Dec-1994 #sequence_revision 01-Sep-1995 #text_change 24-Sep-1999
 C:Accession: S44346
 R:Masutani, C.; Sugawara, K.; Yanagisawa, J.; Sonoyama, T.; Ui, M.; Enomoto, T.; Taki,
 EMBO J. 13, 1831-1843, 1994
 A:Title: Purification and cloning of a nucleotide excision repair complex involving t
 A:Reference number: S44345; MUID:94222030; PMID:8168482
 A:Accession: S44346
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-409 <MAS>
 A:Cross-references: EMBL:ID1090; NID:9498147; PIDN:BA004652.1; PID:dl005181; PID:9498
 F:1-80/Domain: ubiquitin homolog <UBH>

Query Match 32.7%; Score 625.5; DB 2; Length 409;
 Best Local Similarity 34.8%; Pred. No. 1.5e-34;
 Matches 147; Conservative 83; Mismatches 125; Indels 67; Gaps 11;

QY 1 MKLVTKLGTGHEIRVQPNDTIMAVKKNIEIGKDSYPMGQOLLIFNGKVLKDESTYLE 60
 DB 1 MOUTLTKLQOQFKRIDIDPEYVKALEKIESKGDAPVAGOKLITAGKLIINDTALK 60
 QY 61 ENKVNEDGFLVYMLSKGKT-----SGSTGTSSOHSNTPATROAP---PLEAPQ 106
 DB 61 EYKIDKNNVYVAVTPKAVSTPATROASASTTAVTSSTTTVAQAPVTPALAP 120
 QY 107 QAP-----QP-PVAPITTSQPEGLPAQAP-----NTHDNA 135
 DB 121 SPASITPASATASSEPAPASAKOEKPAEFPVATSPATDSTGDSKSNLFEDA 180
 QY 136 ASNLISGRANDTIINLMEMGGSGMDKQVORLRAAYNNPEAVYLYSGITVTEI-A 194
 DB 181 TSLALVIGSGSTENNVETIMSG---YEREDVIALRASFPNPDRAVYLLIPGDRSQA 237
 QY 195 VPIGCGAATTTDRAPTGEAGLSGIPNTAPDLFPQASNAGGAGGAPDLFLNNPOFOA 254
 DB 238 VYDPPQAAST--GAPQSSAVAAAAATTT-----ATTITSSGGHLEFLRNQFOFO 287
 QY 255 VREAVHTNPQIQLPMLVELSKONPQILRIENHDEFQLNPEPE-----GEGEDFLD 308
 DB 288 MROIIOONSLPALLQOIGRENPDQLQOISOHEHFIOMLNEPVQEGAGGGGGGGSG 347
 QY 309 QPEDEMPHA--ISVTPPEGEATGRLESGFDRARYTEFLACDRNEELANYLEHAGE 366
 DB 348 GIAEAGSGHMNTYIQVTPQKEALERLKAIGFPEGIVIAQVFACEKNENLANLLOQND 407
 QY 367 ED 368
 DB 408 ED 409

RESULT 8
 S44443
 RAD23 protein homolog2 - human
 N:Alternate names: HHR23A protein
 C:Species: Homo sapiens (man)
 C>Date: 25-Dec-1994 #sequence_revision 01-Sep-1995 #text_change 18-Feb-2000
 C:Accession: S44443; T45076
 R:Masutani, C.; Sugawara, K.; Yanagisawa, J.; Sonoyama, T.; Uj, M.; Enomoto, T.; Takio, EMO J. 13, 1831-1843, 1994
 A:Title: Purification and cloning of a nucleotide excision repair complex involving the
 A:Reference number: S44345; MID:94222030; PMID:8168482

A:Accession: S44443
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-363 <MAS>
 A:Cross-references: EMBL:D1235; NID:q498145; PIDN:BA04767.1; PID:dl005299; PID:q498146
 R:Immerdin, J.; McCreedy, P.; Stiliwagen, S.; Ramirez, M.; Carrano, A.
 A:Submitted to the EMBL Data Library, November 1996
 A:Description: Characterization by genomic sequence analysis of a gene-rich 111 kb regio
 A:Reference number: 222906
 A:Accession: T45076
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-363 <LAN>
 A:Cross-references: EMBL:AD000092; PIDN:AAB51177.1
 A:Experimental source: cell line 5HL2-B; fibroblast
 C:Genetics:
 A:Gene: RAD23A
 A:Map position: 19p13.2
 A:Introns: 24/3; 78/3; 139/2; 158/1; 200/3; 227/1; 271/3; 326/3
 C:Superfamily: unassigned ubiquitin-related proteins; ubiquitin homology
 F3-82/Domains: ubiquitin homology <UBH>

Query Match 31.6%; Score 603.5; DB 2; Length 363;
 Best Local Similarity 33.4%; Pred. No. 3.7e-33;
 Matches 133; Conservative 88; Mismatches 106; Indels 71; Gaps 8;
 QY 3 LTVKTLKGTGHEIRVQPNDTIMAVKKNIEIGKDSYPMGQOLLIFNGKVLKDESTYLE 62
 DB 5 TLKTLQOQFTKIRMEPDETIVKLEKIEAGKGRAPVAGOKLITAGKLIINDVPIRKY 64

QY 63 KVNEDGFLVYMLSKGTSSTGTSSOHSNTPATROAPLEAPQAPVAPT----- 117
 DB 65 RIDKNNVYVAVT--KTKAGOGTS-----APPAAPTAAPESTSPAPTSGMSHP 114
 QY 118 -----TSQPEGLPAQAPNT-----HDNAANLISGRANDTIINLMENG 156
 DB 115 PPAAREDKSPSEESAPDTSPSEYSGSPSSGSGREDAASTLYTSEYETMLTEIMSG 174
 QY 157 GGSMDKQVORLRAAYNNPERAVEYLYSGIPYATIAVPIGCGAANTDRAPTGAGS 216
 DB 175 ---YERERVYALRASYNPHRAVEYLLTGIP-----GSPEEHSVQESQVS 219
 QY 217 GIPTNPDLFLPQASNAGGAGGAPDLFLRNPOFOAVREAVHTNPQIQLPMLVELSKQ 276
 DB 220 EQPATE-----AAGENPLEFLRDPQFOFNROVIOQNPALLPALLOLQGE 265
 QY 277 NPQILRIENHDEFQLNPE-----TEGGEDFLDPEDEMPHAISVPEGEAIG 330
 DB 266 NPQLLOISRHOEQFTOMLNEPPEGLADISYGEVGAIGEAPOMNTYQVTPQKEALE 325
 QY 331 RLESMGFDRARYTEFLACDRNEELANYLEHAGEED 368
 DB 326 RLKALGFPEESLVIAQVFACEKNENLANLSONFDE 363

RESULT 9
 T40115
 uv excision repair protein rad23 homolog - fission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Sep-2000
 C:Accession: T40115; T51298
 R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Taylor, K.; Harris, D.
 A:Submitted to the EMBL Data Library, September 1998
 A:Reference number: 221906
 A:Accession: T40115
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-368 <WOO>
 A:Cross-references: EMBL:AL031788; PIDN:CAA21170.1; GSPDB:GN00067; SPDB:SPBC2D10.12
 A:Experimental source: strain 972h-, cosmid c2D10
 R:Zhao, Y.; Elder, R.T.
 A:Submitted to the EMBL Data Library, July 1999
 A:Description: A fission yeast orthologue (rhp23) of the human nucleotide excision re
 A:Reference number: 225362
 A:Accession: T51298
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-368 <ZHA>
 A:Cross-references: EMBL:AF174293; PIDN:AAD51975.1
 A:Experimental source: strain SP223
 C:Genetics:
 A:Gene: rhp23; SPDB:SPBC2D10.12
 A:Map position: 2
 A:Introns: 23/3; 48/1; 328/3; 351/3
 C:Superfamily: unassigned ubiquitin-related proteins; ubiquitin homology

Query Match 29.4%; Score 561.5; DB 2; Length 368;
 Best Local Similarity 36.0%; Pred. No. 2.5e-30;
 Matches 142; Conservative 70; Mismatches 127; Indels 55; Gaps 12;
 QY 1 MKLVTKLGTGHEIRVQPNDTIMAVKKNIEIGKDSYPMGQOLLIFNGKVLKDESTYLE 60
 DB 1 MNLTFKNLQOQKFVSDVADSKISELK--EKIQQONVEVEROKLIYSGRLADKTVG 58
 QY 61 ENKVNEDGFLVYMLSKGTSSTGTSSOHSNTPATROAPLEAPQAPVAPT--TT 118
 DB 59 ENIKEDQDIEVCVSRPKTSTSPKSA---SPAPN--PPASVEKVEAPASSTVAEST 112
 QY 119 SQPEGLPAQAPNTHDNAASN-----LISGRANDTIINLMEMGGSGMDKQVORALR 170
 DB 113 STTQVAAAAPNPDTTATSEAPIDANTLAVGAQNRVAVENNVENG---YERSEVERAMR 169

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QY 171 AAYNPRAVEYLYSGIP-----VTAETAVPIGGGAGANTTDRAPIGEAGLSGIPNAPL 224
Db 170 AANNNDRAVEYLLTGPEDILNROREESAAALAOQOQSEALAPSTG-----QPA 221
QY 225 DLPEOGA-----SNAGGAGGGLDFELRNNOFOAVRMVHTNPQILPMLVELSKON 277
Db 222 NLEQOALSNENQOEPSNTVGDPLGLSLRIFOPQOLROIVQONPOMLETILLQOIGQGD 281
QY 278 PQLIRLEENHDEFLOLNEPFEGEEDFLDOPEDEMPHA---ISVPEEOEAIGRLES 334
Db 282 PALAQATQNPFAFLQTL-----AEGABG-----ESALPSSGSIQIQTOSESIDRLCQ 331
QY 335 MGFDRAVIEAFIACDRNEELANYLEHAGEED 368
Db 332 LGFDRNIVIOAYLACDKNEELANYLEHGESE 365

RESULT 10
H86296
F309.1 protein - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 24-Nov-2001
C:Accession: H86296
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.M.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
anssen, N.F.; Hughes, B.; Hultzer, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
A.: Li, J.H.; Li, Y.; Lian, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maitl, R.; Marzall,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: H86296
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-113 <STO>
A:Cross-references: GB:AEO05172; NID:94966345; PIDN:AAD34676.1; GSPDB:GN00141
C:Genetics:
A:Map position: 1

Query Match 22.2%; Score 424; DB 2; Length 113;
Best Local Similarity 73.7%; Pred. No. 8.3e-22;
Matches 84; Conservative 16; Mismatches 10; Indels 4; Gaps 3;

QY 258 MVHNPIILQPMLEYSKONPOLRLEENHDEFLOLNEPFEGEED--DFLOPEDEM 315
Db 1 MVNSNPQILQPMLEYSKONPOLRLEENHDEFLOLNEPFEESDSDVDIFDQPDQ-EM 59

QY 316 PHAIVTPEEOEAIGRLESMPDRARVIEAFIACDRNEELANYLEHAGE-ED 368
Db 60 PHSNVTPPEOGEIERLEAMGFDRAYIEAFIACDRNEELANYLEHSDPDED 113

RESULT 11
T27774
hypothetical protein ZK20.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000
C:Accession: T27774
R:Gajasty, S.
submitted to the EMBL Data Library, March 1996
A:Reference number: Z20417
A:Accession: T27774
A>Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: DNA
A:Residues: 1-372 <MIL>
A:Cross-references: EMBL:Z65904; PIDN:CAA93780.1; GSPDB:GN00020; CESP:ZK20.3
A:Experimental source: clone ZK20
C:Genetics:
A:Gene: CESP:ZK20.3
A:Map position: 2

A:introns: 49/2; 73/3; 101/3; 369/3
C:Superfamily: unassigned ubiquitin-related proteins; ubiquitin homology
Query Match 21.2%; Score 405; DB 2; Length 372;
Best Local Similarity 30.0%; Pred. No. 7.8e-20;
Matches 111; Conservative 65; Mismatches 142; Indels 52; Gaps 8;

QY 1 MKLTVKTLKGTHTFEIRVQPDITMAVKNIEIQQKSDYPMGOQLTFNGKVLKDESTLE 60
Db 52 LSVTFRTLVQVNFLEINEDOTIAEVKALVASEKG--DDVAPDLQKILYNGKIILDDSVK 110
QY 61 ENKYNEDGFLVWLSKRTSGTSGTSSQHSNTPATQAPPLPAPOAPPPVAPITTSQ 120
Db 111 EYGDSSKFFVYVMSKRKVEVAPSSVTAAPAEVPVAAAPASNP--APADVAPEAAA- 167
QY 121 PEGIPAPQPTHDMAANSLISGRNVDTIINQLEMGGSGDKDKVORALAAVNNPRAV 160
Db 168 ----PAAEALTDQENVLA-----ITMGIDREQTIALALRAAPNPDRAV 210
QY 181 EYLYSGIPVTAETAVPIGGGAGANTTDRAPIGEAGLSGIPNAPLDFPGASNAGGAGG 240
Db 211 EFLNLGIPDA-----ADQEP-----DLGPEQNIIDVDEGN 242
QY 241 GPIDFLNNNQFOAVRMVHTNPQILPMLVELSKONPOLRLEENHDEFLOLNEPFE 300
Db 243 DDLMLNLMNPOLARIRALIQONPEMLAAVILQAAVNPRLVOTIQQOAFMDLLNGAQ 302
QY 301 GGEEDFLDOPEED-EMPHAISVPEEOEAIGRLES--MGFDRAVIEAFIACDRNEELAA 357
Db 303 GAGAAAGNAPERNPRRHVHLSPSEAAIERIKATVYVNAPEAVVATYACDKNEEAAI 362
QY 358 NYLIEHAGEE 367
Db 363 NFIRSNIDEE 372

RESULT 12
S50507
excision repair protein RAD23 - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein YEL037C
C:Species: Saccharomyces cerevisiae
C>Date: 28-Jan-1995 #sequence_revision 12-May-1995 #text_change 24-Sep-1999
C:Accession: S50507; S30843; A54599; S38547
R:Dietrich, F.S.
submitted to the EMBL Data Library, December 1994
A:Description: The sequence of S. cerevisiae cosmid 8199, 8334, and 9871.
A:Reference number: S50491
A:Accession: S50507
A:Molecule type: DNA
A:Residues: 1-398 <DIE>
A:Cross-references: EMBL:U18779; NID:9603625; PIDN:AAB65005.1; PID:9603642; MIPS:YEL0
R:Milligan, J.T.; Dietrich, F.S.; Hennessey, K.M.; Sehl, P.; Komp, C.; Wel, Y.; Taylo
submitted to the EMBL Data Library, February 1993
A:Reference number: S30812
A:Accession: S30845
A:Molecule type: DNA
A:Residues: 1-398 <MIL>
A:Cross-references: GB:U18779; EMBL:L10830; NID:9603625; PIDN:AAB65005.1; PID:9603642
R:Watkins, J.F.; Sung, P.; Prakash, L.; Prakash, S.
Mol. Cell. Biol. 13, 7757-7765, 1993
A:Title: The Saccharomyces cerevisiae DNA repair gene RAD23 encodes a nuclear protein
A:Reference number: A54599; MUID:94067136; PMID:8246991
A:Accession: A54599
A:Molecule type: DNA
A:Residues: 1-398 <NAT>
A:Cross-references: GB:U25428; NID:9409246; PIDN:AAA16070.1; PID:9409247
R:Meinick, L.; Sherman, F.
J. Mol. Biol. 233, 372-388, 1993
A:Title: The gene clusters ARC and COR on chromosomes 5 and 10, respectively, of Sacc
A:Reference number: S38543; MUID:94016558; PMID:8411151
A:Accession: S38547
A:Molecule type: DNA
A:Residues: 1-276, 'R', 278-398 <MEL>
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B84549
 Probable ubiquitin-like protein [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
 C:Accession: B84549
 R;lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.;
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MIMD:20083487; PMID:10617197
 A:Accession: B84549
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-536 <STO>
 A:Cross-references: GB:AE002093; NID:g4584342; PIDN:AAD25137.1; GSPDB:GN00139
 C:Genetics:
 A:Gene: At2g17190
 A:Map position: 2

Query Match 10.2%; Score 195.5; DB 2; Length 536;
 Best Local Similarity 20.3%; Pred. No. 1.4e-05;
 Matches 110; Conservative 60; Mismatches 170; Indels 201; Gaps 19;

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QY 3 LTVKTLGTHPEIRVQPNPTIMAVKNIIEIQKSTIPWGOQLIFNGKVLKDSSTLEEN 62
   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 20 VNVKCSNGTGFSTYTSLSDFSEFK--ELIAQNSDVPANQORLIYKGRILKDDOTLLSY 76
   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY 63 KVNEDGFLVYVLSKSGKTSSTGTSQHSNTPATROA----- 99
   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 77 GLQADH--YVAVRGFVSPSSAPAAANAGNOTTAPQAVGSNDSSNLGGESLFPGLGNP 134
   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY 100 -----PLEAPQAPOPPVAITTSOPEGLPA--QAPYTHDMAASNLG 142
   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 135 LGGGNMAGLFGSLPRLDAQO--QLAQNPMIREMNTPAIQMLNMPFMSMIMNN 192
   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY 143 RNVDITINQLEMGGSGMDKQVQALRAVYN-----NPERA--VELYSGIPVT 190
   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 193 PQRELVDYRNPDELGHVLDPSILRQLEAARNPELMRMNTDRAMSNIESMPEGFNWL 252
   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY 191 AEI-----AVPIGGGAGANT-----TDRAPTEGA 213
   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 253 RRMENVOEPLIMATMTSENAGNNTSSNPFALLGNQGVTTQGSPTSNNISAPNAETGTP 312
   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY 214 GLSGIPN-----TAPLDLPQASNAG-----GGAG-----G 241
   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 313 NANLPNPGATAGOTTP-----GRTNAGLGGIGLGGIGLGMGADSPLGATPDAS 366
   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY 242 PLDFLRNNPQFQAVREAVHTNPQILLQPMVLVELSKONPQILRLIEBHDEFLQLLNEPREG 301
   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 367 QLSQILQNPAMQSVLSNPQYMN---OLMSLNPQLRSMIDMN--POLREMGNP--- 418
   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY 302 GEGDFLOPPEDEMPHAI----- 319
   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 419 --DFLRQFSSPEMNOQMSLQOSLFSQNRNTAGODPTQGAATANNGLDLIMNFGSL 475
   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY 320 -----SYTPEQEA--IGRLISMGE--DRARYIEAFIACDRNEELANYLLEHAG 365
   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 476 GAGGLSTGNQNPVPEERFAIQLOQLQEMGFYDRAENIRALLATNGNNAVERLLGSIG 535
   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY 366 E 366
   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 536 Q 536
   :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

```

Search completed: November 4, 2002, 02:03:51
 Job time : 26.7555 secs

